

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/720,896B
Source: IFW/6
Date Processed by STIC: 6/21/06

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/720,896B

DATE: 06/21/2006

TIME: 15:21:32

Input Set : A:\67452507.APP
 Output Set: N:\CRF4\06212006\J720896B.raw

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3 <110> APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
4   CHAMPION, BRIAN ROBERT
5   WARD, GEORGE ALBERT
7 <120> TITLE OF INVENTION: CONJUGATE OF A TRANSPORT PROTEIN AND A PROTEIN FOR
8   MODULATION OF NOTCH SIGNALLING
10 <130> FILE REFERENCE: 674525-2007
12 <140> CURRENT APPLICATION NUMBER: 10/720,896B
13 <141> CURRENT FILING DATE: 2003-11-24
15 <150> PRIOR APPLICATION NUMBER: PCT/GB02/02438
16 <151> PRIOR FILING DATE: 2002-05-24
18 <150> PRIOR APPLICATION NUMBER: GB 0112818.0
19 <151> PRIOR FILING DATE: 2001-05-25
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: PatentIn Ver. 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR primer
32   for amplifying HES1 promoter from mouse genomic DNA
34 <400> SEQUENCE: 1
35 ggggtaccct caggcgccgcg ccattggcc                                29
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 29
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR primer
45   for amplifying HES1 promoter from mouse genomic DNA
47 <400> SEQUENCE: 2
48 gaagatctgc ttacgtcctt ttacttgac                                29
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 26
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
58   major late promoter TATA-box motif with BglII and HindIII
59   cohesive ends
61 <400> SEQUENCE: 3
62 gatctgggg gctataaaag ggggta                                26
65 <210> SEQ ID NO: 4

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: 26
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
late promoter TATA-box motif with BglII and HindIII
ve ends
CE: 4
ttttatagc ccccca 26
NO: 5
: 61
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic CBF-1
er tetramer with XhoI and BglII cohesive ends
CE: 5
ggaaacctaa ccgtgggaac ttaaccgtgg gaacttaacc gtgggaactt 60
61
NO: 6
: 61
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic CBF-1
er tetramer with XhoI and BglII cohesive ends
CE: 6
cccacggta agttcccacg gttaagttcc cacggtaag ttcccacgg 60
61
NO: 7
: 39
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic PCR
mer for generating a truncated fragment of
Notch1 cDNA
CE: 7
ccatggcacg caagcgccgg cgcaagtcat 39
NO: 8
: 31
DNA
SM: Artificial Sequence
E:
INFORMATION: Description of Artificial Sequence: Synthetic PCR
mer for generating a truncated fragment of
Notch1 cDNA
CE: 8
taqtccacq qqcqaaqqa t 31

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136 <210> SEQ ID NO: 9
137 <211> LENGTH: 91
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligo
143 annealed to the NIC2202 sequence to remove the stop codon
144 from theNIC2202 fragment of human Notch1 cDNA
146 <400> SEQUENCE: 9
147 cctggcctgt ggaagcaagg aggccaagga cctcaaggca cgaggagaaga agtcccagga 60
148 tggcaaggggc tgcctgctgg acggcggccg c 91
151 <210> SEQ ID NO: 10
152 <211> LENGTH: 95
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligo
158 annealed to the NIC2202 sequence to remove the stop codon
159 from theNIC2202 fragment of human Notch1 cDNA
161 <400> SEQUENCE: 10
162 tcgagcggcc gccgtccagc aggcagccct tgccatcctg ggacttcttc ctccgtgcct 60
163 tgaggtcctt ggcctccttg cttccacagg ccagg 95
166 <210> SEQ ID NO: 11
167 <211> LENGTH: 2556
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <220> FEATURE:
172 <221> NAME/KEY: MOD_RES
173 <222> LOCATION: (891)
174 <223> OTHER INFORMATION: Variable amino acid
176 <400> SEQUENCE: 11
177 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
178 1 5 10 15
180 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
181 20 25 30
183 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
184 35 40 45
186 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
187 50 55 60
189 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
190 65 70 75 80
192 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
193 85 90 95
195 Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
196 100 105 110
198 Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
199 115 120 125
201 Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys
202 130 135 140
  
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204 Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala
 205 145 150 155 160
 207 Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg
 208 165 170 175
 210 Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly
 211 180 185 190
 213 Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala
 214 195 200 205
 216 Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro
 217 210 215 220
 219 Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr
 220 225 230 235 240
 222 His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu
 223 245 250 255
 225 Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys
 226 260 265 270
 228 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr
 229 275 280 285
 231 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn
 232 290 295 300
 234 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn
 235 305 310 315 320
 237 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile
 238 325 330 335
 240 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp
 241 340 345 350
 243 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
 244 355 360 365
 246 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
 247 370 375 380
 249 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
 250 385 390 395 400
 252 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
 253 405 410 415
 255 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
 256 420 425 430
 258 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
 259 435 440 445
 261 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
 262 450 455 460
 264 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
 265 465 470 475 480
 267 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
 268 485 490 495
 270 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
 271 500 505 510
 273 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
 274 515 520 525
 276 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu

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277	530	535	540													
279	Asp	Gly	Pro	Asn	Thr	Tyr	Thr	Cys	Val	Cys	Thr	Glu	Gly	Tyr	Thr	Gly
280	545		550					555				560				
282	Thr	His	Cys	Glu	Val	Asp	Ile	Asp	Glu	Cys	Asp	Pro	Asp	Pro	Cys	His
283										570					575	
285	Tyr	Gly	Ser	Cys	Lys	Asp	Gly	Val	Ala	Thr	Phe	Thr	Cys	Leu	Cys	Arg
286								580		585			590			
288	Pro	Gly	Tyr	Thr	Gly	His	His	Cys	Glu	Thr	Asn	Ile	Asn	Glu	Cys	Ser
289								595		600			605			
291	Ser	Gln	Pro	Cys	Arg	Leu	Arg	Gly	Thr	Cys	Gln	Asp	Pro	Asp	Asn	Ala
292								610		615			620			
294	Tyr	Leu	Cys	Phe	Cys	Leu	Lys	Gly	Thr	Thr	Gly	Pro	Asn	Cys	Glu	Ile
295								625		630			635			640
297	Asn	Leu	Asp	Asp	Cys	Ala	Ser	Ser	Pro	Cys	Asp	Ser	Gly	Thr	Cys	Leu
298										645			650		655	
300	Asp	Lys	Ile	Asp	Gly	Tyr	Glu	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Thr	Gly
301								660		665			670			
303	Ser	Met	Cys	Asn	Ser	Asn	Ile	Asp	Glu	Cys	Ala	Gly	Asn	Pro	Cys	His
304								675		680			685			
306	Asn	Gly	Gly	Thr	Cys	Glu	Asp	Gly	Ile	Asn	Gly	Phe	Thr	Cys	Arg	Cys
307								690		695			700			
309	Pro	Glu	Gly	Tyr	His	Asp	Pro	Thr	Cys	Leu	Ser	Glu	Val	Asn	Glu	Cys
310								705		710			715			720
312	Asn	Ser	Asn	Pro	Cys	Val	His	Gly	Ala	Cys	Arg	Asp	Ser	Leu	Asn	Gly
313								725		730			735			
315	Tyr	Lys	Cys	Asp	Cys	Asp	Pro	Gly	Trp	Ser	Gly	Thr	Asn	Cys	Asp	Ile
316								740		745			750			
318	Asn	Asn	Asn	Glu	Cys	Glu	Ser	Asn	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys
319								755		760			765			
321	Lys	Asp	Met	Thr	Ser	Gly	Ile	Val	Cys	Thr	Cys	Arg	Glu	Gly	Phe	Ser
322								770		775			780			
324	Gly	Pro	Asn	Cys	Gln	Thr	Asn	Ile	Asn	Glu	Cys	Ala	Ser	Asn	Pro	Cys
325								785		790			795			800
327	Leu	Asn	Lys	Gly	Thr	Cys	Ile	Asp	Asp	Val	Ala	Gly	Tyr	Lys	Cys	Asn
328								805		810			815			
330	Cys	Leu	Leu	Pro	Tyr	Thr	Gly	Ala	Thr	Cys	Glu	Val	Val	Leu	Ala	Pro
331								820		825			830			
333	Cys	Ala	Pro	Ser	Pro	Cys	Arg	Asn	Gly	Gly	Glu	Cys	Arg	Gln	Ser	Glu
334								835		840			845			
336	Asp	Tyr	Glu	Ser	Phe	Ser	Cys	Val	Cys	Pro	Thr	Ala	Gly	Ala	Lys	Gly
337								850		855			860			
339	Gln	Thr	Cys	Glu	Val	Asp	Ile	Asn	Glu	Cys	Val	Leu	Ser	Pro	Cys	Arg
340								865		870			875			880
W--> 342	His	Gly	Ala	Ser	Cys	Gln	Asn	Thr	His	Gly	Xaa	Tyr	Arg	Cys	His	Cys
343								885		890			895			
345	Gln	Ala	Gly	Tyr	Ser	Gly	Arg	Asn	Cys	Glu	Thr	Asp	Ile	Asp	Asp	Cys
346								900		905			910			
348	Arg	Pro	Asn	Pro	Cys	His	Asn	Gly	Gly	Ser	Cys	Thr	Asp	Gly	Ile	Asn
349								915		920			925			

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 891

VERIFICATION SUMMARY

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L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:880